

Gene set enrichment analysis

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 An abbreviated version of this protocol was published in eLIFE in Feb 2022

Application of ATAC-Seq for genome-wide analysis of the chromatin state at single myofiber resolution

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Detailed protocol

A consensus peak set is derived from the uninjured myofibers and MuSCs peaks using DiffBind v.2.16.2 (Stark, 2011, <https://doi.org/10.18129/B9.bioc.DiffBind>). This consensus peak set includes peaks that are present in at least 2 libraries, and is used as input for the differential accessible regions analysis between the uninjured myofiber and MuSCs conditions, using edgeR v.3.30.1 (Robinson et al., 2010, <https://doi.org/10.1093/bioinformatics/btp616>). For each peak, the log2FC, the p-value and the adjusted p-value are calculated. Each peak is then annotated by its nearest gene using the annotatePeaks.pl function of Homer v.4.11 (Heinz et al., 2010, <https://doi.org/10.1016/j.molcel.2010.05.004>). The peaks (regions) and their nearby gene are ranked based on the log2FC prior to the Gene Set Enrichment Analysis. The ranked list of genes is used as input to perform Gene Set Enrichment Analysis with the fgseaMultilevel function of the R package fgsea v.1.14.0 (Korotkevich et al., 2021, <https://doi.org/10.1101/060012>)

How to cite: (Readers should cite both the Bio-protocol preprint and the original research article where this protocol was used)

1. Soleimani, V. D. and Sahinyan, K. (2023). Gene set enrichment analysis. Bio-protocol Preprint. bio-protocol.org/prep2220.
2. Sahinyan, K., Blackburn, D. M., Simon, M., Lazure, F., Kwan, T., Bourque, G. and Soleimani, V. D. (2022). Application of ATAC-Seq for genome-wide analysis of the chromatin state at single myofiber resolution. eLIFE. DOI: [10.7554/eLife.72792](https://doi.org/10.7554/eLife.72792)

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